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RAW SEQUENCE LISTING

DATE: 12/04/2001

PATENT APPLICATION: US/09/851,410A

TIME: 12:15:47

Input Set : N:\Crf3\RULE60\09851410A.txt

Output Set: N:\CRF3\12042001\I851410A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Reyes, Gregory R
6 Yarbough, Patrice O
7 Bradley, Daniel W
8 Krawczynski, Krzysztof Z
9 Tam, Albert
10 Fry, Kirk E

ENTERED

12 (ii) TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
13 Non-A/Non-B Hepatitis Viral Agent

15 (iii) NUMBER OF SEQUENCES: 20

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Dehlinger & Associates
19 (B) STREET: 350 Cambridge Avenue, Suite 250
20 (C) CITY: Palo Alto
21 (D) STATE: CA
22 (E) COUNTRY: USA
23 (F) ZIP: 94306

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk
27 (B) COMPUTER: IBM PC compatible
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/09/851,410A
C--> 33 (B) FILING DATE: 07-May-2001

59 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 09/128,275
37 (B) FILING DATE: 1998-08-03
40 (A) APPLICATION NUMBER: US 07/681,078
41 (B) FILING DATE: 05-APR-1991
44 (A) APPLICATION NUMBER: US 07/505,888
45 (B) FILING DATE: 05-APR-1990
48 (A) APPLICATION NUMBER: US 07/420,921
49 (B) FILING DATE: 13-OCT-1989
52 (A) APPLICATION NUMBER: US 07/367,486
53 (B) FILING DATE: 16-JUN-1989
56 (A) APPLICATION NUMBER: US 07/336,672
57 (B) FILING DATE: 11-APR-1989
60 (A) APPLICATION NUMBER: US 07/208,997
61 (B) FILING DATE: 17-JUN-1988

63 (viii) ATTORNEY/AGENT INFORMATION:

64 (A) NAME: Petithory, Joanne R.
65 (B) REGISTRATION NUMBER: 42,995
66 (C) REFERENCE/DOCKET NUMBER: 4600-0183.24

68 (ix) TELECOMMUNICATION INFORMATION:

69 (A) TELEPHONE: (650) 324-0880

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70          (B) TELEFAX: (650) 324-0960
72 (2) INFORMATION FOR SEQ ID NO: 1:
74   (i) SEQUENCE CHARACTERISTICS:
75       (A) LENGTH: 1295 base pairs
76       (B) TYPE: nucleic acid
77       (C) STRANDEDNESS: double
78       (D) TOPOLOGY: linear
W--> 80   (ii) MOLECULE TYPE: DNA
82   (iii) HYPOTHETICAL: NO
84   (iv) ANTI-SENSE: NO
86   (vi) ORIGINAL SOURCE:
87       (C) INDIVIDUAL ISOLATE: 1.33 kb EcoRI insert of ET1.1,
88           forward sequence
90   (ix) FEATURE:
91       (A) NAME/KEY: CDS
92       (B) LOCATION: 1..1293
94   (ix) FEATURE:
95       (A) NAME/KEY: CDS
96       (B) LOCATION: 2..1294
98   (ix) FEATURE:
99       (A) NAME/KEY: CDS
100      (B) LOCATION: 3..1295
103   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
105 AGACCTGTCC CTGTTGCAGC TGTCTACCA CCCTGCCCGG AGCTCGAACA GGGCCTTCTC      60
107 TACCTGCCCC AGGAGCTCAC CACCTGTGAT AGTGTCGTAA CATTGAATT AACAGACATT      120
109 GTGCACTGCC GCATGGCCGC CCGAGCCAG CGCAAGGCCG TGCTGTCCAC ACTCGTGGGC      180
111 CGCTACGGCG GTCGCACAAA GCTCTACAAT GCTTCCCACT CTGATGTTTC CGACTCTCTC      240
113 GCCCGTTTTT TCCCGGCCAT TGGCCCCGTA CAGGTTACAA CTTGTGAATT GTACGAGCTA      300
115 GTGGAGGCCA TGGTCGAGAA GGGCCAGGAT GGCTCCGCCG TCCTTGAGCT TGATCTTTGC      360
117 AACCCTGACG TGTCCAGGAT CACCTTCTTC CAGAAAGATT GTAACAAGTT CACCACAGGT      420
119 GAGACCATTG CCCATGGTAA AGTGGGCCAG GGCATCTCGG CCTGGAGCAA GACCTTCTGC      480
121 GCCCTCTTTG GCCCTTGGTT CCGCGCTATT GAGAAGGCTA TTCTGGCCCT GCTCCCTCAG      540
123 GGTGTGTTTT ACGGTGATGC CTTTGATGAC ACCGTCTTCT CCGCGGCTGT GGCCGCAGCA      600
125 AAGGCATCCA TGGTGTTTGA GAATGACTTT TCTGAGTTTG ACTCCACCCA GAATAACTTT      660
127 TCTCTGGGTC TAGAGTGTGC TATTATGGAG GAGTGTGGGA TGCCGCAGTG GCTCATCCGC      720
129 CTGTATCACC TTATAAGGTC TGCCTGGATC TTGCAGGCCG CGAAGGAGTC TCTGCGAGGG      780
131 TTTTGGAAGA AACACTCCGG TGAGCCCGGC ACTCTTCTAT GGAATACTGT CTGGAATATG      840
133 GCCGTTATTA CCCACTGTTA TGACTTCCGC GATTTTCAGG TGGCTGCCTT TAAAGGTGAT      900
135 GATTTCGATAG TGCTTTGCAG TGAGTATCGT CAGAGTCCAG GAGCTGCTGT CCTGATCGCC      960
137 GGCTGTGGCT TGAAGTTGAA GGTAAGTTTC CGCCCGATCG GTTTGTATGC AGGTGTTGTG      1020
139 GTGGCCCCCG GCCTTGGCGC GCTCCCTGAT GTTGTGCGCT TCGCCGGCCG GCTTACCGAG      1080
141 AAGAATTGGG GCCCTGGCCC TGAGCGGGCG GAGCAGCTCC GCCTCGCTGT TAGTGATTTC      1140
143 CTCCGCAAGC TCACGAATGT AGCTCAGATG TGTGTGGATG TTGTTTCCCG TGTTTATGGG      1200
145 GTTTCCCCTG GACTCGTTCA TAACCTGATT GGCATGCTAC AGGCTGTTGC TGATGGCAAG      1260
147 GCACATTTCA CTGAGTCAGT AAAACCAAGT CTGGA      1295
150 (2) INFORMATION FOR SEQ ID NO: 2:
152   (i) SEQUENCE CHARACTERISTICS:
153       (A) LENGTH: 431 amino acids
154       (B) TYPE: amino acid

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155          (D) TOPOLOGY: linear
157      (ii) MOLECULE TYPE: protein
159      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
161 Arg Pro Val Pro Val Ala Ala Val Leu Pro Pro Cys Pro Glu Leu Glu
162   1          5          10          15
164 Gln Gly Leu Leu Tyr Leu Pro Gln Glu Leu Thr Thr Cys Asp Ser Val
165          20          25          30
167 Val Thr Phe Glu Leu Thr Asp Ile Val His Cys Arg Met Ala Ala Pro
168          35          40          45
170 Ser Gln Arg Lys Ala Val Leu Ser Thr Leu Val Gly Arg Tyr Gly Gly
171          50          55          60
173 Arg Thr Lys Leu Tyr Asn Ala Ser His Ser Asp Val Arg Asp Ser Leu
174   65          70          75          80
176 Ala Arg Phe Ile Pro Ala Ile Gly Pro Val Gln Val Thr Thr Cys Glu
177          85          90          95
179 Leu Tyr Glu Leu Val Glu Ala Met Val Glu Lys Gly Gln Asp Gly Ser
180          100         105         110
182 Ala Val Leu Glu Leu Asp Leu Cys Asn Arg Asp Val Ser Arg Ile Thr
183          115         120         125
185 Phe Phe Gln Lys Asp Cys Asn Lys Phe Thr Thr Gly Glu Thr Ile Ala
186          130         135         140
188 His Gly Lys Val Gly Gln Gly Ile Ser Ala Trp Ser Lys Thr Phe Cys
189 145         150         155         160
191 Ala Leu Phe Gly Pro Trp Phe Arg Ala Ile Glu Lys Ala Ile Leu Ala
192          165         170         175
194 Leu Leu Pro Gln Gly Val Phe Tyr Gly Asp Ala Phe Asp Asp Thr Val
195          180         185         190
197 Phe Ser Ala Ala Val Ala Ala Ala Lys Ala Ser Met Val Phe Glu Asn
198          195         200         205
200 Asp Phe Ser Glu Phe Asp Ser Thr Gln Asn Asn Phe Ser Leu Gly Leu
201          210         215         220
203 Glu Cys Ala Ile Met Glu Glu Cys Gly Met Pro Gln Trp Leu Ile Arg
204 225         230         235         240
206 Leu Tyr His Leu Ile Arg Ser Ala Trp Ile Leu Gln Ala Pro Lys Glu
207          245         250         255
209 Ser Leu Arg Gly Phe Trp Lys Lys His Ser Gly Glu Pro Gly Thr Leu
210          260         265         270
212 Leu Trp Asn Thr Val Trp Asn Met Ala Val Ile Thr His Cys Tyr Asp
213          275         280         285
215 Phe Arg Asp Phe Gln Val Ala Ala Phe Lys Gly Asp Asp Ser Ile Val
216          290         295         300
218 Leu Cys Ser Glu Tyr Arg Gln Ser Pro Gly Ala Ala Val Leu Ile Ala
219 305         310         315         320
221 Gly Cys Gly Leu Lys Leu Lys Val Asp Phe Arg Pro Ile Gly Leu Tyr
222          325         330         335
224 Ala Gly Val Val Val Ala Pro Gly Leu Gly Ala Leu Pro Asp Val Val
225          340         345         350
227 Arg Phe Ala Gly Arg Leu Thr Glu Lys Asn Trp Gly Pro Gly Pro Glu
228          355         360         365

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230 Arg Ala Glu Gln Leu Arg Leu Ala Val Ser Asp Phe Leu Arg Lys Leu
231      370                      375                      380
233 Thr Asn Val Ala Gln Met Cys Val Asp Val Val Ser Arg Val Tyr Gly
234 385                      390                      395                      400
236 Val Ser Pro Gly Leu Val His Asn Leu Ile Gly Met Leu Gln Ala Val
237      405                      410                      415
239 Ala Asp Gly Lys Ala His Phe Thr Glu Ser Val Lys Pro Val Leu
240      420                      425                      430
243 (2) INFORMATION FOR SEQ ID NO: 3:
245     (i) SEQUENCE CHARACTERISTICS:
246         (A) LENGTH: 18 base pairs
247         (B) TYPE: nucleic acid
248         (C) STRANDEDNESS: single
249         (D) TOPOLOGY: linear
W--> 251     (ii) MOLECULE TYPE: DNA
253     (iii) HYPOTHETICAL: NO
255     (iv) ANTI-SENSE: NO
257     (vi) ORIGINAL SOURCE:
258         (C) INDIVIDUAL ISOLATE: linker - top (5') sequence
260     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
262 GGAATTCGCG GCCGCTCG                                     18
265 (2) INFORMATION FOR SEQ ID NO: 4:
267     (i) SEQUENCE CHARACTERISTICS:
268         (A) LENGTH: 20 base pairs
269         (B) TYPE: nucleic acid
270         (C) STRANDEDNESS: single
271         (D) TOPOLOGY: linear
W--> 273     (ii) MOLECULE TYPE: DNA
275     (iii) HYPOTHETICAL: NO
277     (iv) ANTI-SENSE: NO
279     (vi) ORIGINAL SOURCE:
280         (C) INDIVIDUAL ISOLATE: linker - bottom (3') sequence
282     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
284 CGAGCGGCCG CGAATTCCTT                                     20
286 (2) INFORMATION FOR SEQ ID NO: 5:
288     (i) SEQUENCE CHARACTERISTICS:
289         (A) LENGTH: 1295 base pairs
290         (B) TYPE: nucleic acid
291         (C) STRANDEDNESS: double
292         (D) TOPOLOGY: linear
W--> 294     (ii) MOLECULE TYPE: DNA
296     (iii) HYPOTHETICAL: NO
298     (iv) ANTI-SENSE: NO
300     (vi) ORIGINAL SOURCE:
301         (C) INDIVIDUAL ISOLATE: 1.33 kb EcoRI insert of ET1.1,
302                      reverse sequence
305     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
307 TCGAGCACTG GTTTTACTGA CTCAGTGAAG TGTGCCTTGC CATCAGCAAC AGCCTGTAGC      60
309 ATGCCAATCA GGTATGTAAC GAGTCCAGGG GAAACCCCAT AAACACGGGA AACAACATCC      120

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311 ACACACATCT GAGCTACATT CCTGAGCTTG CGGAGGAAAT CACTAACAGC GAGGCGGAGC 180
313 TGCTCCGCCC GCTCAGGGCC AGGGCCCCAA TTCTTCTGGG TAAGCGGGCC GGCGAAGCCG 240
315 ACAACATCAG GGAGCGCGCC AAGGCCGGGG GCCACCACAA CAGCTGCATA CAAACCGATC 300
317 GGCGGGAAAT CTACCTTCAA CTTCAGGCA CAGCGGGCGA TCAGGACAGC AGCTCCTGGA 360
319 CTCTGACGAT ACTCACTGCA AAGCACTATC GAATCATCAC CTTTAAAGGC AGCCACCTGA 420
321 AAATCGCGGA AGTCATAACA GTGGGTAATA ACGGCCATAT TCAGACAGT ATTCCATAGA 480
323 AGAGTGCCGG GCTCACCGGA GTGTTTCTTC CAAAAACCTC GCAGAGACTC CTTCGGGGCC 540
325 TGCAAGATCC ACGCAGACCT TATAAGGTGA TACAGGCGGA TGAGCCACTG CGGCATCCCA 600
327 CACTCCTCCA TAATAGACA CTCTAGACCC AGAGAAAAGT TATTCTGGGT GGAGTCAAAC 660
329 TCAGAAAAGT CATTCTCAAA CACCATGGAT GCTTTGCTG CGGCCACAGC CGCCGAGAAG 720
331 ACGGTGTCAT CAAAGGCATC ACCGTAAAAAC ACACCTTGAG GGAGCAGGGC CAGAATAGCC 780
333 TTCTCAATAG CGCGGAACCA AGGGCCAAAG AGGGCGCAGA AGGTCTTGCT CCAGGCCGAG 840
335 ATGCCCTGGC CCACTTTACC ATGGGCAATG GTCTACCTG TGGTGAACCT GTTACAATCT 900
337 TTCTGGAAGA AGGTGATCCT GGACACGTCA CGGTGCAAAA GATCAAGCTC AAGGACGGCG 960
339 GAGCCATCCT GCCCTTCTC GACCATGGCC TCCACTAGCT CGTACAATTC ACAAGTTGTA 1020
341 ACCTGTACGG GCCCAATGGC CGGGATAAAA CGGGCGAGAG AGTCGCGAAC ATCAGAGTGG 1080
343 GAAGCATTGT AGAGCTTTGT GCGACCGCCG TAGCGGCCCA CGAGTGTGGA CAGCACGGCC 1140
345 TTGCGCTGGC TCGGGGCGGC CATGCGGCAG TGCACAATGT CTGTTAATTC AAATGTTACG 1200
347 ACACTATCAC AGGTGGTGAG CTCTGGGGC AGGTAGAGAA GGCCCTGTTC GAGCTCGGGG 1260
349 CAGGTGTTA GAACAGCTGC AACAGGGACA GGTCT 1295
352 (2) INFORMATION FOR SEQ ID NO: 6:
354 (i) SEQUENCE CHARACTERISTICS:
355 (A) LENGTH: 7195 base pairs
356 (B) TYPE: nucleic acid
W--> 367 (C) STRANDEDNESS: HEV - Burma strain
358 (D) TOPOLOGY: linear
W--> 360 (ii) MOLECULE TYPE: DNA
362 (iii) HYPOTHETICAL: NO
364 (iv) ANTI-SENSE: NO
366 (vi) ORIGINAL SOURCE:
369 (ix) FEATURE:
370 (A) NAME/KEY: CDS
371 (B) LOCATION: 28..5106
373 (ix) FEATURE:
374 (A) NAME/KEY: CDS
375 (B) LOCATION: 5147..7126
377 (ix) FEATURE:
378 (A) NAME/KEY: CDS
379 (B) LOCATION: 5106..5474
382 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
384 AGGCAGACCA CATATGTGGT CGATGCCATG GAGGCCCATC AGTTTATTAA GGCTCCTGGC 60
386 ATCACTACTG CTATTGAGCA GGCTGCTCTA GCAGCGGCCA ACTCTGCCCT GGCGAATGCT 120
388 GTGGTAGTTA GGCCTTTTCT CTCTCACCAG CAGATTGAGA TCCTCATTA CTAATGCAA 180
390 CCTCGCCAGC TTGTTTTTCCG CCCCAGAGTT TTCTGGAATC ATCCCATCCA GCGTGTGATC 240
392 CATAACGAGC TGGAGCTTTA CTGCCGCGCC CGCTCCGGCC GCTGTCTTGA AATTGGCGCC 300
394 CATCCCGGCT CAATAAATGA TAATCCTAAT GTGGTCCACC GCTGCTTCCT CCGCCCTGTT 360
396 GGGCGTGATG TTCAGCGCTG GTATACTGCT CCCACTCGCG GGCGGGCTGC TAATTGCCGG 420
398 CGTTCCGCGC TGCGCGGGCT TCCGCTGCT GACCGCACTT ACTGCCTCGA CGGTTTTTCT 480
400 GGCTGTAACT TTCCGCGCGA GACTGGCATC GCCCTCTACT CCCTTCATGA TATGTACCA 540

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VERIFICATION SUMMARY

DATE: 12/04/2001

PATENT APPLICATION: US/09/851,410A

TIME: 12:15:48

Input Set : N:\Crif3\RULE60\09851410A.txt

Output Set: N:\CRF3\12042001\I851410A.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:80 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:251 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:273 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:294 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:367 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:367 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=6
L:360 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:1142 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:1142 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=10
L:1135 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:1403 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:1403 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=11
L:1396 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:1477 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:1477 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=12
L:1470 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
L:1651 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:1651 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=17
L:1680 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:1680 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=18
L:1708 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:1708 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=19
L:1736 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:1736 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=20